

## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L.~~et al.~~
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
  - (A) ADDRESSEE: Dr. Kathleen L. Horwath
  - (B) STREET: Department of Biological Sciences, Binghamton University
  - (C) CITY: Binghamton
  - (D) STATE: New York
  - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
  - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
  - (B) COMPUTER: IBM AT/ATX compatible
  - (C) OPERATING SYSTEM: Windows 95/98
  - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
  - (A) APPLICATION NUMBER: 60210446
  - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
  - (A) NAME: Mark Levy, Attorney-at-Law
  - (B) REGISTRATION NUMBER: 29,188
  - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
  - (A) TELEPHONE: 607-722-6600
  - (B) TELEFAX: 607-724-2207

09876348-090901

RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 1

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Peptide
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) FRAGMENT TYPE: N-terminal fragment
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY:
  - (B) CLONE:
- (ix) FEATURES:
  - (D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.8k
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val  
1 5 10 15

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## (2) INFORMATION FOR SEQ. ID NO: 2

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 566 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 13.17
- (vii) FEATURES
  - (D) OTHER INFORMATION: Non-his-tagged, signal plus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTGGATCCAA AGAATTGGC ACGAGACTAC TAAG ATG AAG TTG CTC	36
Met Lys Leu Leu	
	-15

TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG	81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu	
	-10
	-5
	1

ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT	126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys	
	5
	10
	15

CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC	171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg	
	20
	25
	30

AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT	216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe	
	35
	40
	45

TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG	261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val	
	50
	55
	60

GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC	306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn	
	65
	70
	75

GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA	351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg	
	80
	85
	90

GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG	396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met	
	95
	100
	105

AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCAAGA	439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *	
	110
	115

CTAGTAGATG GTTCAAATGG TGTGCTTAC ATATAAAAAT AAAGTGTTC	489
--	-----

TGATGTAAAA AAAAAAAA AAAAAAAA AAATCGAGAG TATTCTAGAG	539
--	-----

CGGCCGCGGG CCCATCGTT TCCACCC	566
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090701-050201



(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys  
 1 5 10 15

Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn  
 20 25 30

Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val  
 35 40 45

Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp  
 50 55 60

Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr  
 65 70 75 80

Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu  
 85 90 95

Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe  
 100 105 110

Ser Pro Val Asp \*  
 115

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(2) INFORMATION FOR SEQ\_ID NO: 5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.2
- (ix) FEATURES
  - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 5:

TCGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC  
 Met Lys Leu Leu Cys Phe Ala Ala Phe Ala Ala  
 -15 -10  
 ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5  
 91  
 AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20  
 136  
 CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35  
 181  
 CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50  
 226  
 GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65  
 271  
 AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80  
 316  
 CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT  
 Gln Lys Cys Val Val Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95  
 361  
 GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110  
 406  
 ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAAT AAAGGTAATA  
 Ile Asp \*  
 115  
 455  
 TCGTTATGTA AAAAAAAAAA AAAAAA  
 481

## (2) INFORMATION FOR SEQ. ID NO: b

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 482 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2-3
- (ix) FEATURES
  - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: b:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46	
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala		
-15	-10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91	
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys		
-5	1	5
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136	
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser		
10	15	20
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181	
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp		
25	30	35
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226	
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly		
40	45	50
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTC CTC AAA GCC	271	
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala		
55	60	65
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG	316	
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val		
70	75	80
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361	
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr		
85	90	95
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406	
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro		
100	105	110
ATT GAT TAA TTGTTTGTAA TTGACTGAA TTTTGACAAT AAAGGTTACTA	455	
Ile Asp *		
115		
TCGTTATGAA AAAAAAAA AAAAAA	482	

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## (2) INFORMATION FOR SEQ. ID NO: ?

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*

- (B) INDIVIDUAL/ISOLATE: none

- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA

- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: ?

Met	Lys	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala	Ile	Val	Ile	Gly	Ala
-15							-10						-5	

Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys
1					5							10			

Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val
15				20					25					30	

Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	Pro	Lys	Met	Lys	Lys	His	Val	Leu
				35				40					45		

Cys	Phe	Ser	Lys	Lys	Thr	Gly	Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn
				50				55				60			

Val	Glu	Val	Leu	Lys	Ala	Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu
	65						70					75			

Val	Asp	Lys	Ile	Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu
	80				85					90					

Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp
95					100				105			110			

Phe	Ser	Pro	Ile	Asp	*										
	115														

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(2) INFORMATION FOR SEQ. ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: OR

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and

(vii) IMMEDIATE SOURCE:

(B) CLONE: 2.2, 2

#### (ix) FEATURES

(D) OTHER INFORMATION: Mature Prot

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
1 5 10 15

Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
35 40 45

Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
50 55 60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
85 90 95

Ala Tyr Asp Thr

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(2) INFORMATION FOR SEQ. ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged. Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	4b	
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala		
-15	-10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91	
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys		
-5	1	5
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	13b	
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser		
10	15	20
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181	
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp		
25	30	35
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226	
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly		
40	45	50
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271	
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala		
55	60	65
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	31b	
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val		
70	75	80
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361	
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr		
85	90	95
GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	40b	
Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro		
100	105	110
ATT GAT TAA TTGTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTTACTA	455	
Ile Asp *		
115		
TCGTTATGTA AAAAAAAA AAAAAA	481	

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(2) INFORMATION FOR SEQ\_ID NO: 10

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 133 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.4
- (ix) FEATURES
  - (D) OTHER INFORMATION: Precursor Protein for Clone 3.4
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 10:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-75 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp

Phe Ser Pro Ile Asp \*

1134

RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 Amino Acids

(B) TYPE: Amino Acid

### (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3

## (ix) FEATURES

(D) OTHER INFORMATION: Mature Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
1 5 10 15

Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
35 40 45

Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
50 55 60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
85 90 95

Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
100 105 110

Pro Ile Asp \*

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## (2) INFORMATION FOR SEQ. ID NO: 12

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 482 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.9
- (ix) FEATURES
  - (D) OTHER INFORMATION: Non-His-tagged, Signal plus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	4b
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala	
-15	-10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA	91		
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys			
-5	1		5
	5		

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC	13b		
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser			
10	15		20
	20		

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181		
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp			
25	30		35
	35		

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA	22b		
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly			
40	45		50
	50		

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTC CTC AAA GCC	271		
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala			
55	60		65
	65		

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG	31b		
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val			
70	75		80
	80		

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	3b1		
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr			
85	90		95
	95		

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	40b		
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro			
100	105		110
	110		

ATT GAT TAA TTGTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTTACTA	455
Ile Asp *	
115	

TCGTTATGAA AAAAAAAAAA AAAAAAAA	482
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(2) INFORMATION FOR SEQ. ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: DR

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none  
(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

## (ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein for Clone 3.9  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

WWW.SOURCEFORUM.COM 800.877.3223

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
-15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp

Phe Ser Pro Ile Asp \*

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(2) INFORMATION FOR SEQ. ID NO: 14

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 115 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.9
- (ix) FEATURES
  - (D) OTHER INFORMATION: Mature protein for Clone 3.9
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys  
1 5 10 15

Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr  
20 25 30

Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe  
35 40 45

Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu  
50 55 60

Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp  
65 70 75 80

Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr  
55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70

Ala-Tyr-Asp-Thr-Phe-Lys-Cys-Tle-Tyr-Asp-Ser-Lys-Phe-Asp-Phe-Ser

Res. 116, App. \*

115

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## (2) INFORMATION FOR SEQ. ID NO: 15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GGCACGAGCA	AAA	ATG	AAA	CTC	CTC	TTG	TGC	TTT	GCG	TTC	GCC	GCC	4b
Met	Lys	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala				
													-10
													-15

ATC	GTC	ATC	GGA	GCT	CAG	GCT	CTC	ACC	GAC	GAA	CAG	ATA	CAG	AAA	90
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	
														-5	
														1	
														5	

AGG	AAC	AAG	ATC	AGC	AAA	GAG	TGC	CAG	CAG	GTG	TCC	GGA	GTG	TCC	13b
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	
														10	
														15	
														20	

CAA	GAG	ACG	ATC	GAC	AAA	GTC	CGC	ACA	GGT	GTC	TTG	GTC	GAC	GAT	181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	
														25	
														30	
														35	

CCC	AAA	ATG	AAG	AAG	CAC	GTC	CTC	TGC	TTC	TCG	AAG	AAA	ACT	GGA	22b
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	
														40	
														45	
														50	

GTG	GCA	ACC	GAA	GCC	GGG	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	GCC	271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	
														55	
														60	
														65	

AAG	CTG	AAG	CAT	GTG	GCC	AGC	GAC	GAA	GAG	GTG	GAC	AAG	ATC	GTG	31b
Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val	
														70	
														75	
														80	

CAG	AAG	TGC	GTG	GTC	AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	TAT	36b
Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Thr	Ala	Tyr		
														85	
														90	
														95	

GAC	ACC	TTC	AAG	TGT	ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	CCT	40b
Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	Pro	
														100	
														105	
														110	

ATT	GAT	TAA	TTG	TTT	GTG	TAA	TTT	GGCTGAA	TTT	TGACAAT	AAAGGTACTA	455	
Ile	Asp	*											
		115											

TCGTTATGTA	AAAAAAAAAAA	AAAAAAA	481
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## (2) INFORMATION FOR SEQ. ID NO: 16

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vi) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus

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RB125 RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

## (2) INFORMATION FOR SEQ. ID NO: 17

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 169 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.2
- (ix) FEATURES
  - (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
 -40 -35 -30 -20 -15

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala  
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
 105 110 115

T02090-B4E94860

## (2) INFORMATION FOR SEQ. ID NO: 18

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.2
- (ix) FEATURES
  - (D) OTHER INFORMATION: His-tagged, signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG 50

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC 9b  
 Met Gly Ser Ser His His His His His His His Ser  
 -30 -25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141  
 Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly  
 -20 -15 -10

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 18b  
 Gly Gln Gin Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
 -5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231  
 Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
 10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT 27b  
 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
 25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT 321  
 Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr  
 40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA 366  
 Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys  
 55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411  
 Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile  
 70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 45b  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
 85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCA CCACGTGAGAT 543  
 Pro Ile Asp \*  
 115

T01/0890-84452860

23

## (2) INFORMATION FOR SEQ. ID NO: 19

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 149 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2-2
- (ix) FEATURES
  - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
 95 100 105 110

Phe Ser Pro Ile Asp \*  
 115

FD2090-84E9Z860

(2) INFORMATION FOR SEQ. ID NO: 20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 662 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.3
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal Plus

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

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(2) INFORMATION FOR SEQ. ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
 -40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala  
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
 -10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
 10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
 40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
 55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
 75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
 90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
 105 110 115

070708090810081108120813081408150816081708180819081A081B081C081D081E081F081G081H081I081J081K081L081M081N081O081P081Q081R081S081T081U081V081W081X081Y081Z081

## (2) INFORMATION FOR SEQ\_ID NO: 22

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.3
- (ix) FEATURES
  - (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 22:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
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AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	-25

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	-30

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	-5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	-10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	-25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	-40 45 50

GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTC CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	-55 60 65

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	-70 75 80

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	-85 90 95

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	-100 105 110

CCT ATT GAT TAA CTCGAGCACC ACCACCA CCACGTGAGAT	543
Pro Ile Asp *	115

T02090-BHE90-007897890

## (2) INFORMATION FOR SEQ. ID NO: 23

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.3

## (ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met	Gly	Ser	Ser	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
														-20

-30

-25

Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg
															-5

-15

-10

-5

Gly	Ser	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	Lys
															10

1

5

10

Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	Gln	Glu	Thr	Ile	Asp	Lys	Val
															30

15

20

25

Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	Pro	Lys	Met	Lys	Lys	His	Val	Leu
															45

35

40

45

Cys	Phe	Ser	Lys	Lys	Thr	Gly	Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn
															60

50

55

60

Val	Glu	Val	Leu	Lys	Ala	Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu
															75

65

70

75

Val	Asp	Lys	Ile	Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu
															80

80

85

90

Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp
															110

95

100

105

Phe	Ser	Pro	Ile	Asp	*
					115

470 471 472 473 474 475 476 477 478 479 480

(2) INFORMATION FOR SEQ. ID NO: 24

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 777 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 13.17
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal plus

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His His Ser -65 -60 -55	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -50 -45 -40	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT Gly Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile -35 -30 -25	186
CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser -20 -15 -10	231
CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile -5 1 5	276
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly 10 15 20	321
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu 25 30 35	366
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn 40 45 50	411
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu 55 60 65	456
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu 70 75 80	501
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu 85 90 95	546
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys 100 105 110	595
TTC TCA CCA GTT GAT TGA ACCACCACTGA CTAGTAGATG GTTCAAATGG Phe Ser Pro Val Asp *	643
TGTGCTTAC ATATAAAAT AAAGTGTTC TGATGTAAAA AAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	693
TCCACCCCTC GAGCACCAC ACCACCACTGA CTGAGAT	743

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(2) INFORMATION FOR SEQ\_ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 25:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile  
 -25 -20 -15 -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile  
-5 1 5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val  
10 15 20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp  
25 30 35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu  
40 45 50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val  
55 60 65 70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys  
75 80 85

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp \*

105 110 115

(2) INFORMATION FOR SEQ. ID NO: 2b

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2b:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG 50

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AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC 96
          Met Gly Ser Ser His His His His His His Ser
          -30          -25

```

```

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT      141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-20          -15          -10

```

GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA 186  
 Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys  
 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100

CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG 231  
 Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser  
 10 15 20

CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT 27b  
 Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp  
 35 35 35 35 35 35 35 35 35 35 35 35 35 35 35

```

CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT 321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly
          Val Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly

```

```

AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC 411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile

```

ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG 45b  
 Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val

TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA 501  
 Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser

CCA GTT GAT TGA CTCGAGCACC ACCACCAACCA CCACTGAGAT 543  
Pro Val Asp \*

(2) INFORMATION FOR SEQ. ID NO: 27

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 149 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 13.17
- (ix) FEATURES
  - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys  
1 5 10 15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg

35 40 45

50 55 60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu  
65 70 75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu  
80 85 90 95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys

Phe Ser Pro Val Asp \*

RB125 RT

## (2) INFORMATION FOR SEQ. ID NO: 28

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 681 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.4
- (vii) FEATURES
- (viii) OTHER INFORMATION: His-tagged, Signal plus

09876348 . 060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT AGC Met Gly Ser Ser His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly. Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	186
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -10 -5	231
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser 1 5 10	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTC CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val 90 95 100	546
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	595
105 110 115	
TTTGACTGAA TTTTGACAAAT AAAGGTACTA TCGTTATGTA AAAAAAAA	645
AAAAAAACTCG AGCACCCACCA CCACCAACAC TGAGAT	681

DRAFT 2/8/2000

## (2) INFORMATION FOR SEQ\_ID NO: 29

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 173 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.4
- (ix) FEATURES
  - (D) OTHER INFORMATION: Precursor protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 29:

Met Gly Ser Ser His His His His Ser Ser Gly Leu Val Pro  
                           -55                          -50                  -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
                           -40                          -35                  -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Phe Ala  
                           -25                          -20                  -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
                           -10                          -5                      1                  5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
                           10                          15                      20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
                           25                          30                      35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
                           40                          45                      50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
                           55                          60                      65                      70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
                           75                          80                      85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
                           90                          95                      100

Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp \*  
                           105                          110                      115

40704 6060708 8090708 00708 3040708 708708 408708

(2) INFORMATION FOR SEQ\_ID NO: 30

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.4
- (ix) FEATURES
  - (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 30:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50

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AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC      96
      Met Gly Ser Ser His His His His His His Ser
      -30          -25

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```

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-20 -15 -10

```

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG 186  
 Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
 -5 1 5

```

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG 231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
 10          15          20

```

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276  
 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
 25 30 35

```

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC 411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Val Asp Lys Ile
          20          25          30          35          40

```

GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT 45b  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
~~EF~~ ~~EF~~ ~~EF~~ ~~EF~~ ~~EF~~ ~~EF~~

TAT GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT 501  
 Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143

CCT ATT GAT TAA CTCGAGCACC ACCACCAACCA CCACTGAGAT 543  
Pro Ile Asp \*

(2) INFORMATION FOR SEQ. ID NO: 31

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vi) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

#### (ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp  
 95 100 105 110

Phe Ser Pro Ile Asp \*

115

RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 32

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 682 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.9
- (ix) FEATURES
  - (D) OTHER INFORMATION: His-tagged, Signal plus

09876348-090701

RB125 RT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

(2) INFORMATION FOR SEQ\_ID NO: 33

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 173 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.9
- (ix) FEATURES
  - (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 33:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 -55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
 -25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Pro Ile Asp \*  
105 110 115

(2) INFORMATION FOR SEQ\_ID NO: 34

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.9
- (ix) FEATURES
  - (D) OTHER INFORMATION: His-tagged; Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 34:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTGT TTACTTTAAG 50

```

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC 96
          Met Gly Ser Ser His His His His His Ser
          -30          -25

```

```

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
          -20          -15          -10

```

GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CAG 186  
 Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln  
 -5 1 5

AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG 231  
 Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val  
 10 15 20

TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC 276  
 Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp  
 25 30 35

GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT 321  
 Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr  
 up up 50

GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC 411  
 Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Glu Val Asp Lys Ile  
 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60

GTC CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT . 45b  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Lys Thr Ala .  
 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65

TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 125 150 175 200 225 250 275 300 325 350 375 390 415	

CCT ATT GAT TAA CTCGAGCACC ACCACCAACCA CCACTGAGAT 543  
Pro Ile Asp \*

(2) INFORMATION FOR SEQ\_ID NO: 35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 149 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 3.9
- (ix) FEATURES
  - (D) OTHER INFORMATION: Mature Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 35:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
95 100 105 110

Phe Ser Pro Ile Asp \*

(2) INFORMATION FOR SEQ. ID NO: 3b

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 681 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 7.5
- (vii) FEATURES
- (viii) OTHER INFORMATION: His-tagged, Signal plus

09876348, 060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGTTAGCGG	ATGGAATTCC	CTCGTAGGGG	ATAATTTGT	TTACTTTAAG	50
AGGAGATAT	ACC ATG GGC	AGC AGC CAT	CAT CAT CAT	CAT CAC AGC	96
Met Gly	Ser Ser His	Ser His His His	His His His His	Ser Ser Ser Ser	
-55	-50	-45	-40	-35	
AGC GGC CTG GTG CGG CGC	GGC AGC CAT ATG GCT	AGC ATG ACT GGT			141
Ser Gly Leu Val Pro Arg	Gly Ser His Met Ala	Ser Met Thr Gly			
-45	-40	-35	-30	-25	
GGA CAG CAA ATG GGT CGC	GGG TCC GAA TTC GCA	CGA GCA AAA ATG			186
Gly Gln Gln Met Gly Arg	Gly Ser Glu Phe Ala	Arg Ala Lys Met			
-30	-25	-20	-15	-10	
AAA CTC CTC TTG TGC TTT	GCG TTC GCC GCC ATC	GTC ATC GGA GCT			231
Lys Leu Leu Leu Cys Phe	Ala Phe Ala Ala Ile	Val Ile Gly Ala			
-15	-10	-5	-15	-10	
CAG GCT CTC ACC GAC GAA	CAG ATA CAG AAA AGG	AAC AAG ATC AGC			276
Gln Ala Leu Thr Asp Glu	Gln Ile Gln Lys Arg	Asn Lys Ile Ser			
1	5	10	15	20	
AAA GAG TGC CAG CAG GTG	TCC GGA GTG TCC CAA GAG	ACG ATC GAC			321
Lys Glu Cys Gln Gln Val	Ser Gly Val Ser Gln	Glut Thr Ile Asp			
15	20	25	15	20	
AAA GTC CGC ACA GGT GTC	TTG GTC GAC GAT CCC AAA ATG	AAG AAC			366
Lys Val Arg Thr Gly Val	Leu Val Asp Asp Pro	Lys Met Lys Lys			
30	35	40	30	35	
CAC GTC CTC TGC TTC TCG	AAG AAA ACT GGA GTG	GCA ACC GAA GGC			411
His Val Leu Cys Phe Ser	Lys Lys Thr Gly Val	Ala Thr Glu Ala			
45	50	55	45	50	
GGA GAC ACC AAT GTG GAG	GTA CTC AAA GCC AAG	CTG AAG CAT GTG			456
Gly Asp Thr Asn Val Glu	Val Leu Lys Ala Lys	Leu Lys His Val			
60	65	70	60	65	
GCC AGC GAC GAA GAG GTG	GAC AAG ATC GTG CAG	AAG TGC GTG GTC			501
Ala Ser Asp Glu Glu Val	Asp Lys Ile Val Gln	Lys Cys Val Val			
75	80	85	75	80	
AAG AAG GCC ACA CCA GAG	GAA ACG GCT TAT GAC	ACC TTC AAG TGT			546
Lys Lys Ala Thr Pro Glu	Glu Thr Ala Tyr Asp	Thr Phe Lys Cys			
90	95	100	90	95	
ATT TAC GAC AGT AAA CCT	GAT TTC TCT CCT ATT	GAT TAA TTGTTTTGTA			595
Ile Tyr Asp Ser Lys Pro	Asp Phe Ser Pro Ile	Asp *			
105	110	115	105	110	
TTGGCTGAA TTTGACAAT	AAAGGTACTA	TCGTTATGTA	AAAAAAAAAAA		645
AAAAAACTCG	AGCACCAACCA	CCACCAACAC	TGAGAT		

AAAAAACTCG AGCACCAACCA CCACCAACAC TGAGAT 681

(2) INFORMATION FOR SEQ\_ID NO: 37

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 173 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 7.5
- (ix) FEATURES
  - (D) OTHER INFORMATION: Precursor Protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 37

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala  
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile  
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val  
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val  
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu  
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys  
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys  
90 95 100

(2) INFORMATION FOR SEQ. ID NO: 38

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 543 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 7.5
- (ix) FEATURES
  - (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTGT TTA	CTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC		9b
Met Gly Ser Ser His His His His His His Ser		
-30		
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT		141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly		
-20	-15	-10
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG		18b
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln		
-5	1	5
AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG		231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val		
10	15	20
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC		27b
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp		
25	30	35
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT		321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr		
40	45	50
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GAA GTC CTC AAA		36b
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys		
55	60	65
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC		411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile		
70	75	80
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA AGC GCT		45b
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala		
85	90	95
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT		501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser		
100	105	110
CCT ATT GAT TAA CTCGAGCACC ACCACCA CCACTGAGAT		543
Pro Ile Asp *		
115		

## (2) INFORMATION FOR SEQ. ID NO: 39

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 147 Amino Acids
  - (B) TYPE: Amino Acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Protein
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 7.5
- (ix) FEATURES
  - (D) OTHER INFORMATION: Mature protein with His-tag
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 -30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg  
 -15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu  
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu  
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp  
 95 100 105 110

Phe Ser Pro Ile Asp \*  
 115

TOP SECRET - 843527800

(2) INFORMATION FOR SEQ. ID NO: 40

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
- (ix) FEATURES
  - (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-H1 site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG 24

09876348 .060701

(2) INFORMATION FOR SEQ ID NO: 41

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
- (ix) FEATURES
- (D) OTHER INFORMATION: Tm 12.84 lower primer with Xhol site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAAA CTAATTGAGC TCGCC 25

09876348.060701

(2) INFORMATION FOR SEQ. ID NO: 42

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 13.17
- (ix) FEATURES
  - (D) OTHER INFORMATION: Tm 13-17 upper primer with Bam-H1 site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA 24

09876348 . 060701

RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 43

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 13.17
- (vii) FEATURES
  - (D) OTHER INFORMATION: Tm 13.17° lower primer with Xhol site
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAACTGAGC TCGCC 25

Y027090 "84E947860

(2) INFORMATION FOR SEQ. ID NO: 44

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.2
- (ix) FEATURES
  - (D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCN TTC GCC GCC 46  
 Met Lys Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAY GAA CAG ATA CAG AAA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

AGG AAC AAG ATC AGC AAA GAR TGC CAG CAG GNG TCC GGA GTG TCC 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAY GAT 181  
 Gin Gln Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG ARA ACT GGA 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTC CTC AAA GCC 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAR GTG GAC AAG ATC GTG 316  
 Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val  
 70 75 80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT 361  
 Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr  
 85 90 95

GAC ACC TTC AAG NNT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT 406  
 Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro  
 100 105 110

ATT GAT TAA TTGTTTGTA TTGRCGTGAA TTTTGACAAT AAAGGTANTAA 455  
 Ile Asp \*  
 115

TCGTTATGNA AAAAAAAAAA AAAAAA 481

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(2) INFORMATION FOR SEQ\_ID NO: 45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vi) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2.2
- (ix) FEATURES
  - (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17
- (xi) SEQUENCE DESCRIPTION: SEQ\_ID NO: 45:

GGCANRNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYC NYC RYY 46  
                   Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala  
                   -15                         -10

NTN NTN RTC RNA GYT CAG GCY CTN ACC GAN GNA CAR ATN NAG AAA  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

NNG AAC AAG ATC AGC AAA RAR TGY CAR NAN GNR NNY GGA GTG TCN	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	

CAA GAG AYN ATN RNC AAA GYY CGC ANN GGT GNC TNG GNN GAY GAT 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCY AAA NTG AAR NRN CAN GTY YTY TGC NTN NCN ARG ARN RCY GGN 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
   40           45           50

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NTG GCN ACN GAA NCN GGA GAN RYN RNN GTN GAN GTR YTN ARR GNN 271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Val Leu Lys Ala
55          60          65

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AAG NTG ARG NAN GTN RCY RRC AAC GAC GAA GAR RYN GAN AAR ATC	316
Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile	
70 75 80	

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RTN NAN AAG TGC GYN GTC AAG ARR GNY ACN NYN GAR GAR ACG GYN 361
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala
85 90 95

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TNY RAY ACY TTC AAR NNT RTY NNN RAN ARY AAR CCN RAN TTC TCN 406  
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 300 305 310

CCN RTT GAT TRA NYNNYYNNNA YTNGNNRNR NTTYRANAAT AAAGNNNTN 458  
Pro Ile Asp \*  
115

TNRTNNNRNA AAAAAAAAAA AAAAAAA 484

RB125 RT

(2) INFORMATION FOR SEQ. ID NO: 4b

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 481 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (v)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: *Tenebrio molitor*
  - (B) INDIVIDUAL/ISOLATE: none
  - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: cDNA
  - (B) CLONE: 2-2
- (ix) FEATURES
  - (D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4b:

GGCANNNNN AAR ATG AAR YTN CTC TNN TGY YTN RYN TYY NYC RYY 4b  
 Met Lys Leu Leu Cys Phe Ala Phe Ala Ala  
 -15 -10

NTN NTN RTC NNA GYT CAG GCY NTN ACY NAN GNA NAN NTN NAG NNA 91  
 Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys  
 -5 1 5

NNG NNC NAR AYC AGC RNA RAR TGY NAR NNN GNR NNY GGA GTG TCN 136  
 Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser  
 10 15 20

NAA GAN ATN RNN ARA GYY CGG ANN GGT GNC TNG GNN GAY GAY 181  
 Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp  
 25 30 35

CCY AAA NTG AAR NNN CAN NTY YTY TGC NTN NYN ARG RNN NYV GRN 226  
 Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly  
 40 45 50

NTR GYN RCN GAA NCN GGA GAN RYN RNN GYN GAN RYR YTN ARR GNN 271  
 Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala  
 55 60 65

AAG NTG ANG NRN NNN NNN RNN ANN RNN RAR RAR RYN RRN ARR NTN 316  
 Lys Leu Lys His Val Ala Ser Asn Asp Glu Glu Val Asp Lys Ile  
 70 75 80

YNM NRN ARN NNN NNN NNN NNG ARN RNN NYN NNN RAR RNR NNN NNN 361  
 Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala  
 85 90 95

TNN RAN NYN YYN AAN NNN NNY NNN RRN ANN ARN ARN CCN RNN TYY TYN 406  
 Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser  
 100 105 110

CNN RYT RNT TRN NYNNNNNNN YNNNGNNRNR NTTYRANAAT AAAGNNNYTN 458  
 Pro Ile Asp \*  
 115

TNRTNNNRNA AAAAAAAA AAAAAA 484

## (2) INFORMATION FOR SEQ. ID NO: 47

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*

- (B) INDIVIDUAL/ISOLATE: none

- (C) CELL TYPE: fat body and whole organism

## (vi) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA

- (B) CLONE: 2.2

## (vii) FEATURES

- (D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3

## (viii) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GGC	NNNNNNN	AAR	ATG	AAR	YTN	CTC	YNN	TGY	YTN	RYN	YYY	NYY	RYY	46
		Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala		
													-15	
														-10

NTN	NTN	RYC	NNR	RYY	YAN	GCY	NTN	ACY	NAN	RNA	NNN	NNN	NAG	NNR	91
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	
														-5	
														1	
														5	

NNG	NNY	NAR	NNC	RNN	RNN	TGY	NAR	NNN	GNR	NNY	GGA	GTR	TCN	136
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Glu	Ser	Gly	Val	
														10
														15
														20

NAA	GAN	NYN	NTN	RNN	ARR	GYY	CGC	ANN	NGT	GNN	NNR	GNN	GAY	GAY	181
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Vai	Leu	Val	Asp	Asp	
														25	
														30	
														35	

CCY	AAA	NTG	AAR	NNN	CAN	NYY	TYT	TGC	NTN	YN	ARG	RNN	NYY	GRN	226
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	
														40	
														45	
														50	

NTN	RYN	RNN	GNN	NNN	GGN	GAN	NYN	NNN	YN	GAN	NNN	NNN	ARR	RNN	271
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	
														55	
														60	
														65	

AAR	NTN	ANG	NRN	NNN	NNN	RNN	RNN	NNN	RAR	RAR	RAR	RYN	RRN	RRN	NTN	316
Lys	Leu	Lys	His	Val	Ala	Ser	Asn	Asp	Glu	Glu	Val	Asp	Lys	Ile		
														70		
														75		
														80		

NYN	NNN	ARN	NNN	NNN	NNN	NNG	ARN	RNN	NYN	NNN	NAR	NNN	NNN	NNN	361
Val	Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	
														85	
														90	
														95	

NNN	RAN	NYN	AYN	NNN	NNN	NNY	NNN	RRN	ANN	ARN	YCN	NNN	TNN	NNN	406
Tyr	Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	
														100	
														105	
														110	

CNN	NYN	RNN	TRN	NNNNNNNNN	NNNNNNNNN	NNNNNNNAAT	AAANNNNNNN	458
Pro	Ile	Asp	*					
			115					

NNNNNNNNNN	AAAAAAAAAA	AAAAAA	484
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(2) INFORMATION FOR SEQ. ID NO: 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE:

(ix) FEATURES

(D) OTHER INFORMATION: General Concensus of Clones,  
B1, B2 and AFP-3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  
 Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Ala Ala Thr  
 Thr Leu Val Val -5  
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys  
 Tyr Ile Glu Ala Asp Leu Glu Leu Leu Arg Gln Thr Ala  
 Thr Pro Arg Lys His Asp  
 1 5 10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val  
 Lys Lys Asn Val Ala Glu Asp Ile Leu Thr Arg Ala  
 Ala Thr Ala Val Lys Ser Asn  
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu  
 Asn Arg Asp Trp Glu Leu Arg Gln Leu Phe  
 Lys Glu Glu Met Ala  
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn  
 Val Ala Arg Arg Ala Ile Val Ala Ala Ser Glu Ile Glu  
 Ile Phe Ala Leu Glu Ile Ile Asp Val Val  
 Leu Asn Glu Phe Gln  
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser ^ Asp Glu  
 Ala Asp Thr Phe Arg Glu Val Thr Arg Asn Thr Asn Asp Pro  
 Leu His Ile Thr Phe Arg Lys Ser Asp Asn  
 65 70 75

Glu Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro  
 Lys Ser Glu Asp Leu Ile Glu Ala Thr Glu Asp Val  
 Thr Asn Ala  
 80 85 90

Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro  
 Gln Asp Ser Val Phe Glu Val Thr Val Val Leu Lys Asn Arg Ser  
 His Ser Ala Asn Phe Met Asp His  
 95 100 105 110

Asp Phe Ser Pro Ile Asp ^ ^ ^ \*  
 Asn Phe Gly Asp Leu Phe Val \*  
 Lys Val \*  
 115

0090-8463/87/01